EIC' I **69**5 1000 2322 7322 1984 4899 9146 23130 (qpd) **O**  $\mathbf{B}$  $\forall$ əziZ



Fragment



## FIG.2A

HsKin-mmKin ne	Hskin-mmkin nen 16 10 1997 16 00	00 9		7						
	10	ର-	30	40	20	09	07	8-	6-	100
hsKin17.pep	MGKSDFLIPK AIANRIKSKG LQKLRWYCQM CQKQCRDENG FKCHCMSESH QRQLLLASEN PQQFMDYFSE EFRNDFLELL RRRFGTKRVH NNIVYNEYIS *	INR IKSKG	QKLRWYCQM	CQKQCRDENG	FKCHCMSESH	<b>QRQLLLASEN</b>	PQQFMDYFSE	EFRNDFLELL	RRRFGTKRVH N	INIVYNEYIS
mmKin17.pep	MGKSDFLSPK AIANRIKSKG LOKLRWYCOM COKOCRDENG FKCHCMSESH OROLLLASEN POOFMDYFSE EFRNDFLELL RRRFGTKRVH NNIVYNEYIS	NRIKSKG 1	-QKLRWYCQM	COKOCRDENG	FKCHCMSESH	QRQLLLASEN	POOFMDYFSE	EFRNDFLELL	RRRFGTKRVH N	INIVYNEYIS
;	110	120	130	140	0 150	160	170	180	190	200
hsKin17 . pep	HREHIHMNAT QWETLTDFTK WLGREGLCKV DETPKGWYIQ YIDRDPETIR RQLELEKKKK QDLDDEEKTA KFIEEQVRRG LEGKEGEVPT FTELSRENDE * * *	TLTDFTK	AL GREGL CKV	DETPKGWYIQ	YIDRDPETIR	ROLELEKKKK	QDLDDEEKTA	KF IEEQVRRG	LEGKEQEVPT F * *	TELSRENDE *
mmKin17.pep	HREHIHMNAT QWETLIDFTK WLGREGLCKV DETPKGWYIQ YIDRDPETIR RQLELEKKKK QDLDDEEKTA KFIEEQVRRG LEGKEQETPV FTELSRENEE	TLTDFTK	#LGREGLCKV	DETPKGWYIQ	YIDRDPETIR	ROLELEKKKK	QDLDDEEKTA	KF IEEQVRRG	LEGKEQETPV F	TELSRENEE
	210	220	230	240	0 250	360	270	280	290	300
hsKin17.pep	EKVTFNLSKG ACSSSGATSS KSSTLGPSAL KTIGSSASVK RKESSQSSTQ SKEKKKKKSA LDEIMEIEEE KKRTARTDYW LQPEIIVKII TKKLGEKYHK  * ** * * * * * * * * * * * * * * * *	SSSGATSS	<pre><sstlgpsal *<="" pre=""></sstlgpsal></pre>	KTIGSSASVK ** * **	RKESSQSSTQ **	SKEKKKKKSA ****	LDEIMEIEEE *	KKRTARTDYW *	LQPEIIVKII 1	.KKL GEKYHK
mmKin17 . pep	EKVIFNLNKG AGGSAGATTS KSSSLGPSAL KLLGSAASGK RKESSQSS AQPAKKKKSA LDEIMELEEE KKRTARTDAW LQPGIVVKII TKKLGEKYHK	SAGATTS	KSSSLGPSAL	KLLGSAASGK	RKESSQSS	AQPAKKKKSA	LDEIMELEEE	KKRTARTDAW	LQPGIVVKII	TKKL GEKYHK
	310	320	330	340	0 350	360	370	380	390	400
hsKin17 . pep	KKAIVKEVID KYTAVVKMID SGDKLKLDQT HLETVIPAPG KRILVLNGGY RGNEGTLESI NEKTFSATIV IETGPLKGRR VEGIQYEDIS KLA	TAVVKMID *	SGDKLKLDQT *	HLETVIPAPG	KRILVLNGGY *	RGNEGTLESI	NEKTF SATIV *	IETGPLKGRR	VEGIQYEDIS A	(LA
mmKin17.pep	KKGVVKEVID RYTAVVKMTD SGDRLKLDQT HLETVIPAPG KRVLVLNGGY RGNEGTLESI NEKAFSATIV IETGPLKGRR VEGIQYEDIS KLA	TAVVKMTD	SGDRLKLDQT	HLETVIPAPG	* KRVL VLNGGY	RGNEGTLESI	NEKAFSATIV	IETGPLKGRR	VEGIQYEDIS +	(LA
	410	420	430	) 440	0 450	) 460	470	480	490	500
hsKin17 . pep	1									
mmKin17 , pep	! !! ! \\									
_	_									



## FIG. 2B

hsKin17-mmKin17 16 10 1997 15 59	16 10 1997	15 59								
	10	ਨ 	30	0 40	20	9-	2-	≅-	-	100
hsKin17 . seq	TGATTCGAGC	TCGGTACCCG	GGGATCCGA	TAGAAAGTGA	TGATICGAGC ICGGTACCCG GGGATCCGAT TAGAAAGTGA TCGCTGCCGT GGTCGCCATG GGGAAGTCGG ATTTICTTAC TCCCAAGGCT ATCGCCAACA * * * * * * * * * * * * * * * * * * *	GGTCGCCATG	GGGAAGTCGG *	ATTTCTTAC * *	TCCCAAGGCT *	ATCGCCAACA *
mmKin17.seg						ATG	ATG GGCAAGICGG ATTITCTGAG CCCCAAGGCT ATCGCCAATA	ATTTTCTGAG	CCCCAAGGCT	ATCGCCAATA
	110	120	0 130	30 140	0 150	160	170	180	190	200
hsKin17 . seq	GGATCAAGTC * *	CAAGGGGCTG	CAGAAGCTA(	CCTGGTATTG *	GGATCAAGIC CAAGGGGCIG CAGAAGCIAC GCIGGIAIIG CCAGAIGIGC CAGAAGCAGI GCCGGGACGA GAAIGGCIII AAGIGICAII GIAIGICCGA * * * * * * * * * * * * * * * * * * *	CAGAAGCAGT * *	GCCGGGACGA *	GAATGGCTTT	AAGTGTCATT *	GTATGTCCGA *
mmKin17,seq	GAATTAAGTC	CAAAGGGCTC	CAGAAGCTT(	CCTGGTACTG	GAATTAAGIC CAAAGGGCIC CAGAAGCIIC GCIGGIACIG CCAGAIGIGC CAAAAGCAAT GCCGCGACGA GAAIGGCIII AAGIGICACI GIAIGICIGA	CAAAAGCAAT	GCCGCGACGA	GAATGGCTTT	AAGTGTCACT	GTATGTCTGA
	210	220	). (2)	230 240	0 250	950	270	280	290	300
hsKin17 . seq	ATCTCATCAG *	AGACAACTA1	160166011	C AGAAAATCCT *	ATCTCATCAG AGACAACTAT TGCTGGCTTC AGAAAATCCT CAGCAGTTTA TGGATTATTT TTCAGAGGAA TTCCGAAATG ACTTTCTAGA ACTTCTCAGG * * * * *	TGGATTATTT	TTCAGAGGAA	TTCCGAAATG	ACTTTCTAGA *	ACTTCTCAGG *
mmKin17.seg	ATCTCATCAA	AGACAACTG1	. 160166011	C AGAAAACCCI	ATCICATCAA AGACAACTGT TGCTGGCTTC AGAAAACCCT CAGCAGTTTA TGGATTATTT TTCAGAGGAA TTCCGAAATG ACTTTCTGGA ACTTCTGAGG	TGGATTATTT	TTCAGAGGAA	TTCCGAAATG	ACTTTCTGGA	ACTICTGAGG
-	310	320	33.	330 340	0 350	360	370	380	390	400
hsKin17 . seq	AGACGCTTTG *	GCACTAAAA(	GGTCCACAA	C AACATTGTC1	AGACGCITIG GCACTAAAAG GGICCACAAC AACATIGICI ACAACGAATA CAICAGCCAC CGAGAGCACA ICCACATGAA TGCCACTCAG TGGAAACTC * * * * * * * * * * * * * * * * * * *	CATCAGCCAC	CGAGAGCACA	TCCACATGAA	TGCCACTCAG * * *	TGGGAAACTC * *
mmKin17.seq	CGACGCTTTG	GCACTAAAA(	GGTCCACAA	C AACATTGTC1	CGACGCTITG GCACTAAAAG GGTCCACAAC AACATIGTCT ACAATGAATA CATCAGCCAC CGAGAGCACA ICCACATGAA CGCTACCCAG TGGGAGACAC	CATCAGCCAC	CGAGAGCACA	TCCACATGAA	CGCTACCCAG	TGGGAGACAC
-	410	46	420 43	430 440	10 450	) 460	470	480	490	200
hsKin17 . seq	TGACTGATTI * *	TACTAAGTG	; CTGGGCAGA	G AAGGCTTGT(	TGACTGATTT TACTAAGTGG CTGGGCAGAG AAGGCTTGTG CAAAGTGGAC GAGACACCAA AAGGCTGGTA TATTCAGTAC ATAGACAGGG ACCCAGAAAC	GAGACACCAA	AAGGCTGGTA	TATTCAGTAC *	ATAGACAGGG **	ACCCAGAAAC
mmKin17.seq	TGACCGACTT	TACCAAGTG	j ctgggcaga	G AGGCTTGF(	TGACCGACTT TACCAAGTGG CTGGGCAGAG AGGGCTTGTG TAAAGTGGAT GAGACACCGA AAGGCTGGTA CATTCAGTAC ATAGACAGAG ACCCAGAAAC	GAGACACCGA	AAGGCTGGTA	CATTCAGTAC	ATAGACAGAG	ACCCAGAAAC
	_									



### FIG. 20

	ATCCCCCG	520 CAACTGGAAC *	530 TGGAGAAAA * *	540 GAAAAAGCAG	550 GACCTTGATG * * *	560 ATGAAGAAAA	S70 AACTGCCAAA	580 TTTATTGAAG *	AGCAAGTGAG	510 520 530 540 550 560 570 580 590 600  TATCCGCCGG CAACTGGAAA GAAAAAGCAG GACCTTGATG ATGAAGAAAA AACTGCCAAA TTTATTGAAG AGCAAGTGAG AAGAGGCCTG  * * * * * * * * * * * * * * * * * * *
CATC	36TCGG 610	CGG CAACTGGAAT T 6¦0 620	Tagaaaaaa 630	CATCCGTCGG CAACTGGAAT TAGAAAAAAA GAAGAAGCAA GATCTGGACG ATGAAGAAAA AACTGCCAAG TTCATTGAGG AGCAGGTGAG AAGAGGCCTG 610 620 630 640 650 660 700	SAA GATCTGGACG ATGAAGAAAA AACTGCCAAG TTCATTG 640 650 660 670	ATGAAGAAAA 660	AACTGCCAAG 670	TTCATTGAGG 680	4GG AGCAGGTGAG 690 699	GAG AAGAGGCCTG 690 700
<b>₹</b>	4GGGAAGG *	AACAGGAGGT * **	CCCTACTTTT * **	ACGGAATTAA * * *	GCAGAGAAAA *	TGATGAAGAG * *	AAAGTCACGT *	TTAATTTGAG * * *	TAAAGGAGCA **	GAAGGGAAGG AACAGGAGGT CCCTACTTTT ACGGAATTAA GCAGAGAAAA TGATGAAGAG AAAGTCACGT TTAATTTGAG TAAAGGAGCA TGTAGCTCAT  * * * * * * * * * * * * * * * * * * *
ৣ	AGGGAAAG A 710	AGCAGGAGAC , 720	ACCTGTTTTT	GAAGGGAAAG AGCAGGAGAC ACCTGTTTT ACAGAACTTA GCCGAGAAAA TGAGGAAGAA AAAGTTACGT TCAATCTGAA TAAAGGAGCG GGTGGCTCAG 7¦0 720 730 740 750 8qc	GCCGAGAAAA 750	Tgaggaagaa 760	AAAGTTACGT 770	TCAATCTGAA 780	TAAAGGAGCG	GGTGGCTCAG ) 800
: TS **	CGGAGCAAC *	ATCTTCCAAG * *	TCAAGTACTC ** *	CCGGAGCAAC ATCTTCCAAG TCAAGTACTC TGGGACCGAG TGCACTGAAG ACGATAGGAA GTTCAGCATC AGTGAAACGA AAAGAATCTT CCCAGAGCTC * * * * * * * * * * * * * * * * * * *	TGCACTGAAG	ACGATAGGAA ** * *	GTTCAGCATC **	AGTGAAACGA * * *	AAAGAATCTT *	CCCAGAGCTC *
	IGGAGC TAC	AACATCCAAG	TCAAGCTCTT	CGGGAGCTAC AACATCCAAG TCAAGCTCTT TGGGACCAAG TGCACTGAAG CTGCTGGGGA GCGCAGCATC CGGGAAACGG AAAGAGTCTT CACAGAGCTC	TGCACTGAAG	CTGCTGGGGA	GCGCAGCATC	CGGGAAACGG	AAAGAGTCTT	CACAGAGCTC



# FIG. 2D

hsKin17-mmKin17	
	850 830 840 850 860 870 880 890 900
hsKin17 . seq	AACTCAGTCT AAAGAAAAGA AGAAAAAGAA ATCTGCACTG GATGAAATCA TGGAGATTGA AGAGGAAAAG AAAAGAACTG CCCGAACAGA CTACTGGCTA   ** * * * * * * * * * * * * * * * * *
mmKin17.seq	T. 96
hsKin17 . seq	CAGCCTGAAA TTATTGTGAA AATTATAACC AAGAAACTGG GAGAGAAATA TCATAAGAA AAAGGCTATT GTTAAGGAAG TAATTGACAA ATATACAGCT  * ** ** ** ** * * * * * * * * * * * *
mmKin17.seq	CAGCCGGGA TCGTTGTGAA AATTATAACG AAGAAGCTTG GGGAGAAATA TCACAAGAAG AAAGGGG TC GTTAAGGAAG TGATTGACAG GTACACAGCT
hsKin17 . seq	GITGIGAAGA IGATIGATIC TGGAGACAAG CTGAAACTIG ACCAGACTCA TTTAGAGACA GTAATTCCAG CACCAGGAAA AAGAATTCTA GTTTTAAATG
mmKin17.seq	* * * * * * * *   CIGAGACAGG CIGAAACIGG ACCAGACICA IITAGAGACA GICATICCGG CCCCGGGGAA AAGGGIICIA GITITAAAIG
	1110 1120 1130 1140 1150 1160 1170 1180 1190 1120
hsKin17 . seq	GAGGCTACAG AGGAAATGAA GGTACCCTAG AATCCAICAA IGAGAAGACI IIIILAGLIA LIAILGILAI IGAAATIGAA GGTACCCTAG AATCCAICAA 
mmKin17.seq	GAGGCTACAG AGGAAATGAA GGCACTCTCG AATCCATCAA TGAGAAGGCT ITITCAGCCA CGATAGTCAT TGAAACTGGA CCTTTGAAAG GACGCAGAGT



	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
hskin17 . seq	TGAAGGAATT C	IGAAGGAAII CAATAIGAAG ACAITICTAA ACIIGCCIGA GIIIGAAAAI IIGIIAACAA TACCITIAAA AICI IAAAG CATCAAAIIG GIGIICGC * * * * * * * * * * * * * * * * * * *	ATTICTAA AC *	TTGCCTGA GI	TTGAAAAT	GTTAACAA T.	ACCTTTAAA ATC	T TAAAG CATC * *	AAATTG GTGT	** ** **
mmKin17.seg	TGAAGGTATT C	TGAAGGTATT CAATATGAAG ACATATCTAA ACTTGCTTGA GTTTGAAAAT TTGATAACAA CACA TTGAA A CTGTGAAG CATCAAATTG GTGTTAGCCA	ATATCTAA AC	TTGCTTGA GI	TTGAAAAT Ti	IGATAACAA C.	ACA TTGAA A C	TGTGAAG CATC	AAATTG GTGT	TAGCCA
-	1310	1320	1330	1340	1350	1360	1360 1370 1380	1380	1390	1400
hsKin17 . seq	* ****	**************************************	** ******	(* ***********************************	<b>(* *******</b>	* *********	*** *******	*****	**** *****	****
mmKin17 .seq	AGGCACTGTG 1	AGGCACTGTG TAACTCTACT GTGTTAGGGG ATTTGTTTTG TATTAAAAA AAAAAAATCA TCTATTTAAA TACTAGTGAA TAGTTGGGTA AATTTATAT	GTTAGGGG A1	TIGITITG TA	ATTAAAAA A	AAAAATCA T	CTATTTAAA TAC	TAGTGAA TAGI	itgggta aatt ********************************	TATAAT
	1410	1420	1430	1340	1450	1	1470	1480	1490	00CI
hsKin17 . seq	*****	***************************************	K* ********	.* ******* ****************************	******* *******************************	****				
mmKin17 . seq	AAAATCTATG	AAAATCTATG TTTTTTAA GTGTAAAAAA AAAAAAAAA AAAAAAAA	GTAAAAA AA	AAAAAAA A	AAAAAAAA A	AAAAA				



### FIG. 3A

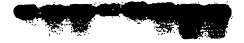
heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas

spleen
thymus
prostate
testicle
ovary
small intestine
colon
peripheral blood leukocyte

Kin-17

β Actin







### FIG. 3B

HL-60 Hela S3 K-562 Molt-4 Raji SW480 A 549 G 361

Kin-17



β Actine





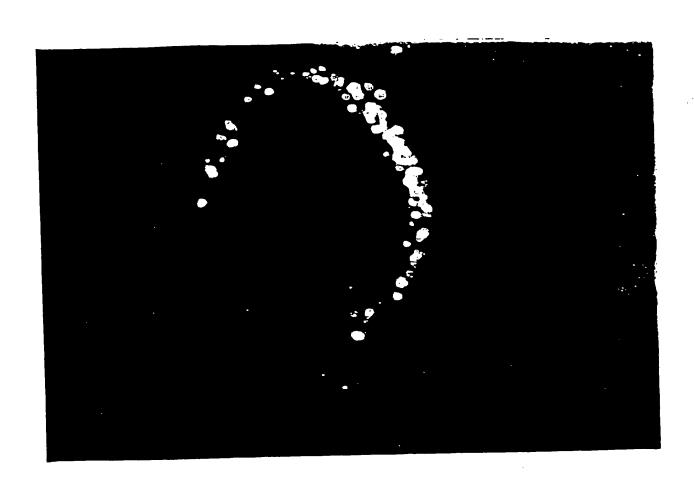


FIG. 4A





FIG. 4B



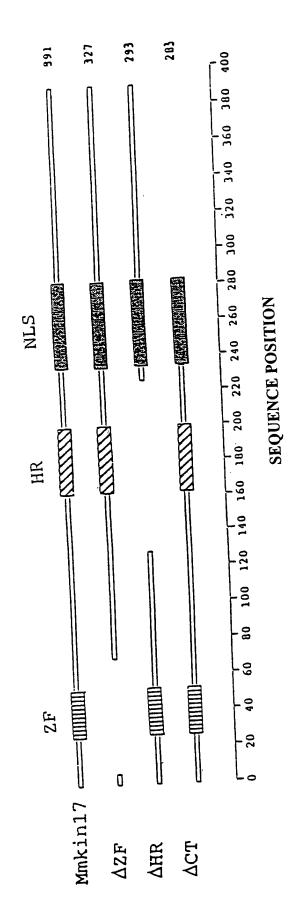


FIG. 5



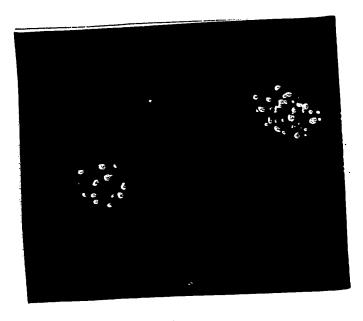


FIG. 6A

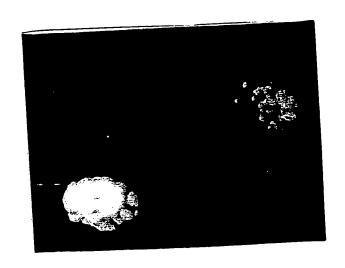


FIG. 6B

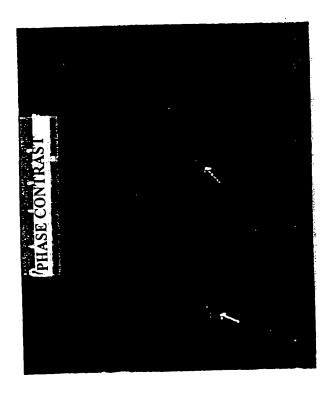


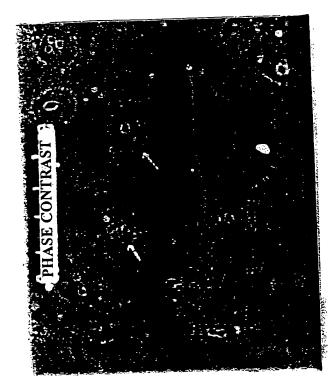














### ग्रीकृतिस्व अस्टि

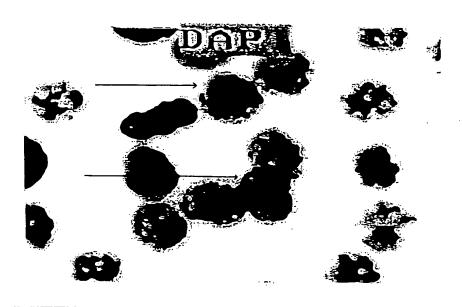


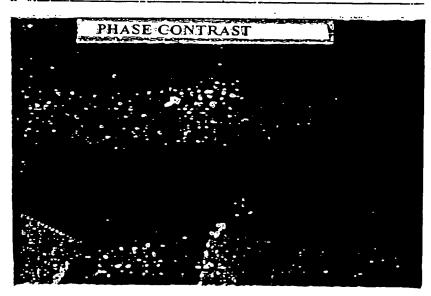


















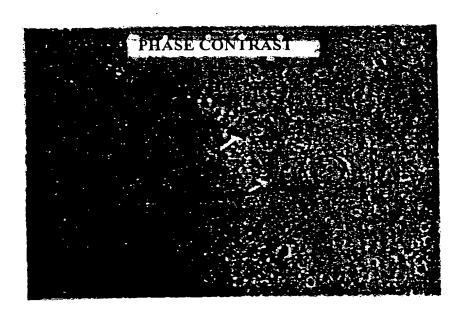
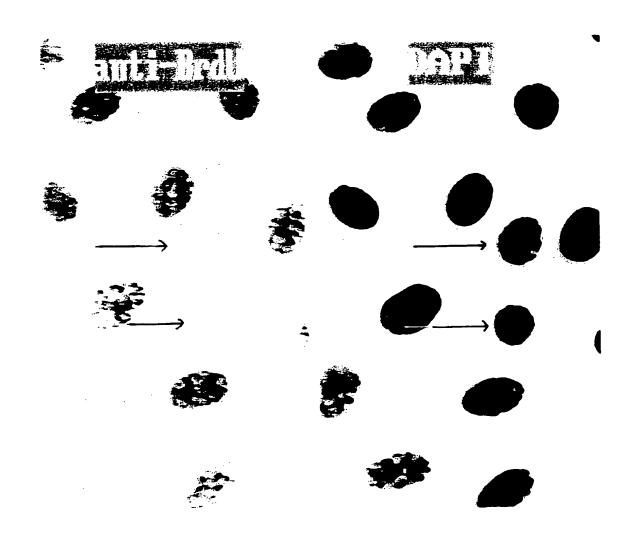


FIG. 9





**FIG. 10A** 



PROTEIN EXPRESSED	NONE	kin17 LOW LEVEL HIC	kin17 LOW LEVEL HIGH LEVEL	kin∆HR	kindCT
% of Cells REPLICATING THEIR DNA	. 40	40	0	0	33

FIG. 10B



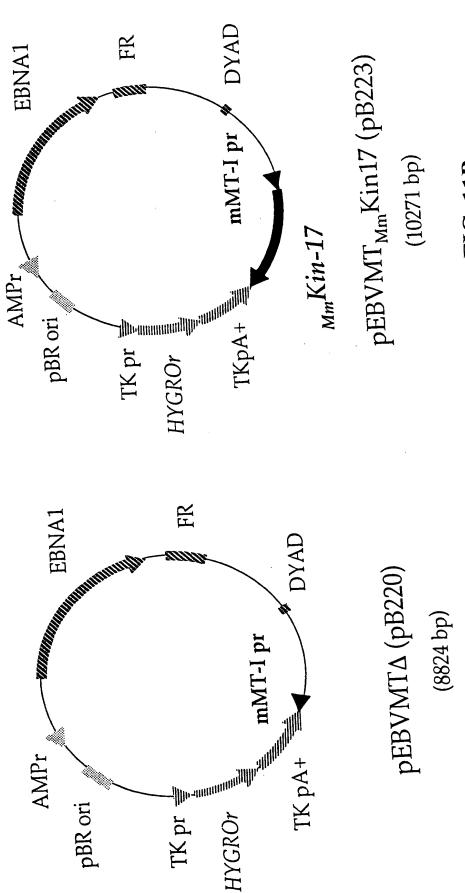


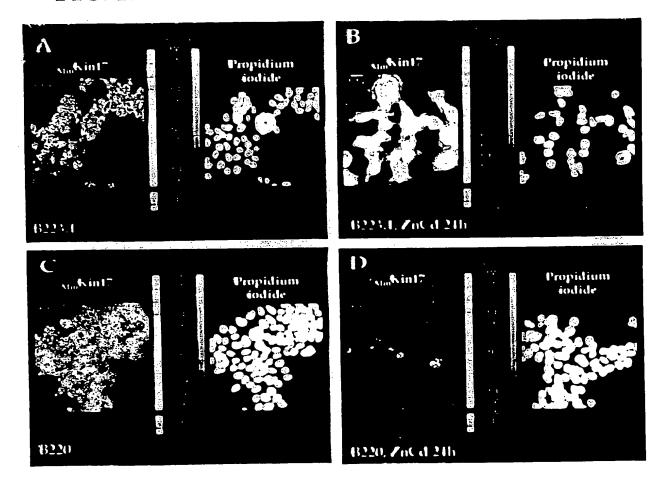
FIG. 11B

FIG. 11A



### **FIG. 12A**

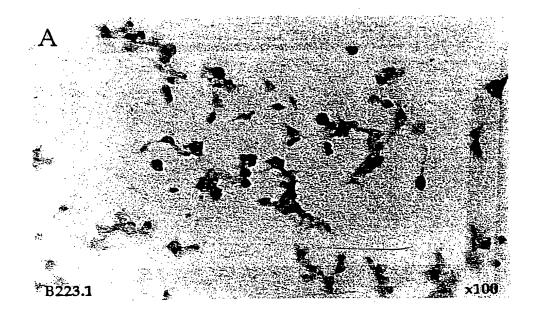
**FIG. 12B** 



**FIG. 12C** 

**FIG. 12D** 





**FIG. 13A** 

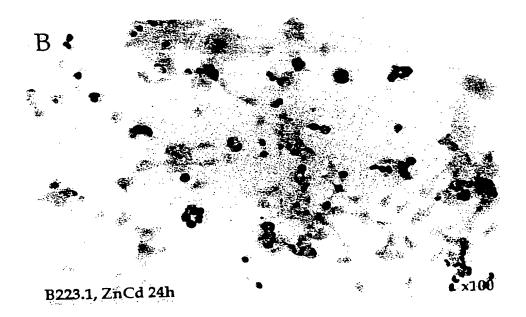
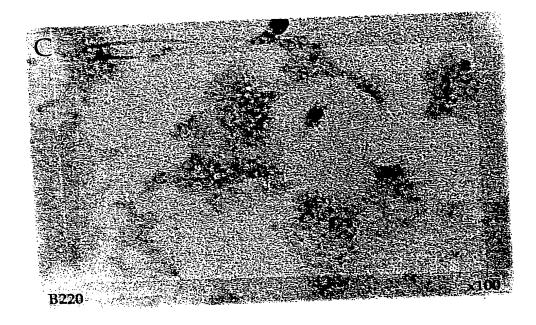
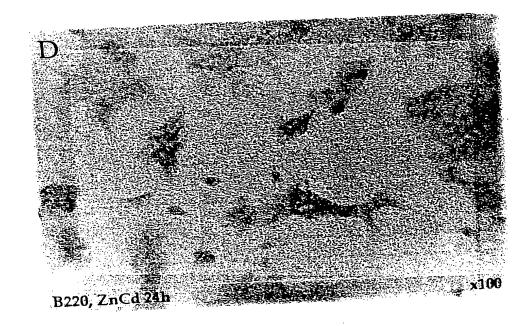


FIG. 13B



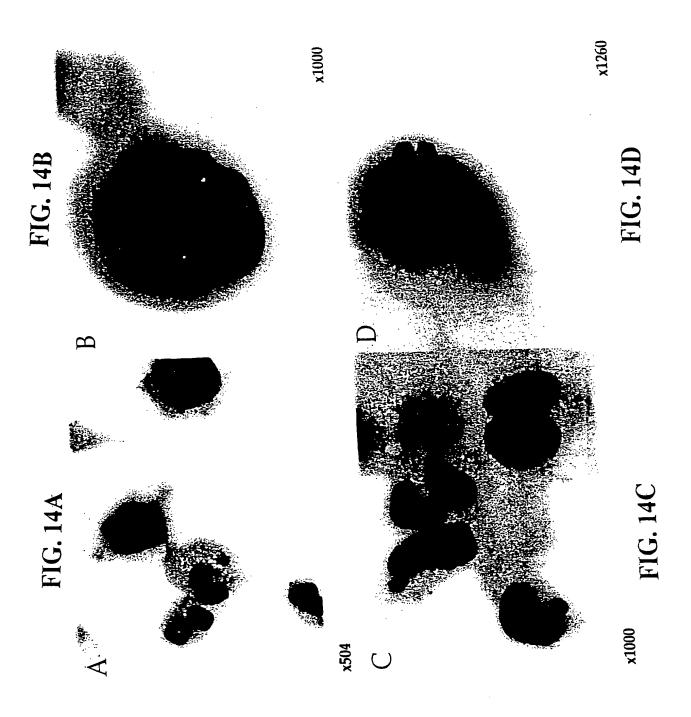


**FIG. 13C** 

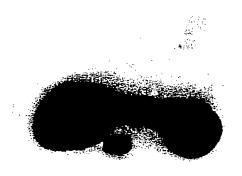


**FIG. 13D** 

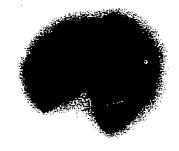








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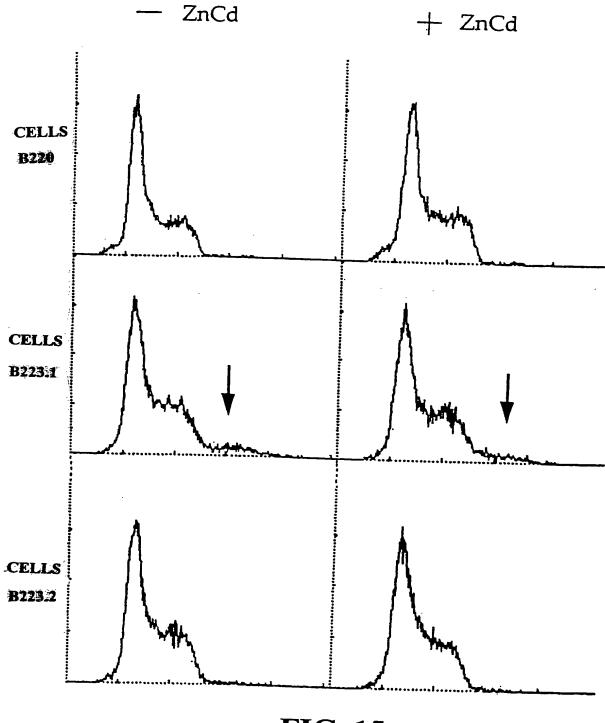
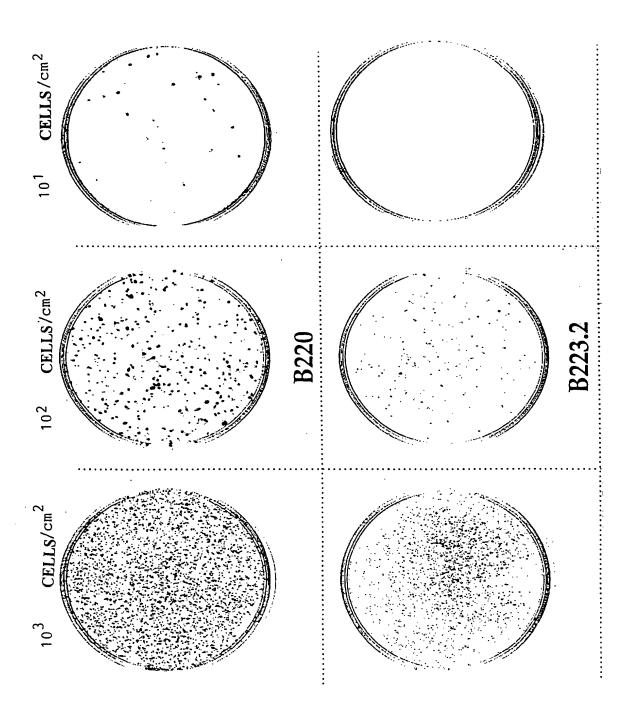


FIG. 15







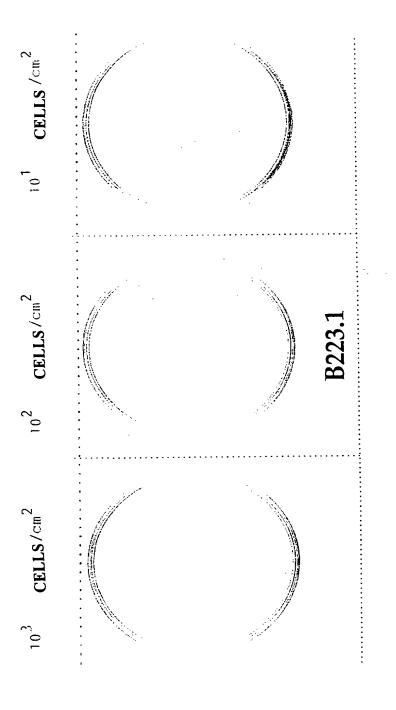


FIG. 16E



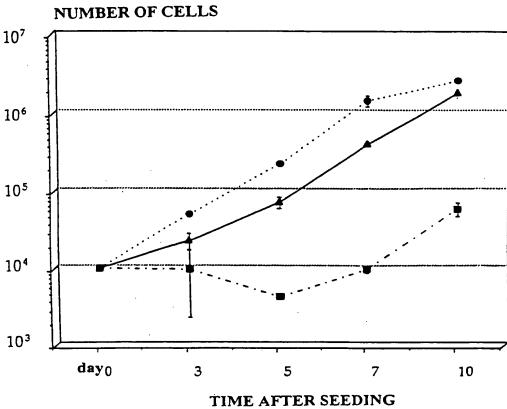
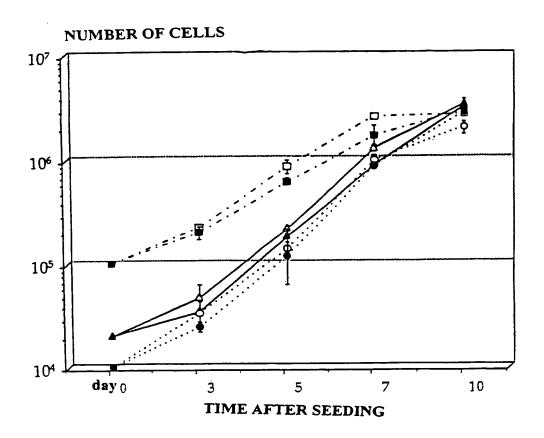
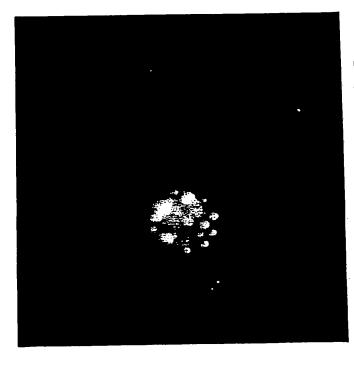


FIG. 17B







GFPkin17NLS-CT FIG. 18B

